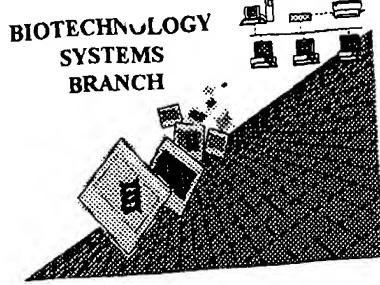


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/766,571

Source: OIPE

Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/766,511

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.

12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/766,511

DATE: 02/05/2001
 TIME: 13:34:38

Input Set : A:\10147_61.txt
 Output Set: N:\CRF3\02052001\I766511.raw

3 <110> APPLICANT: MCCARTHY, Sean A
 4 FRASER, Christopher C
 5 SHARP, John D
 6 BARNES, Thomas S
 7 KIRST, Susan J
 8 MYERS, Paul S
 9 WRIGHTON, Nicholas
 10 GOODEARL, Andrew
 11 HOLTZMAN, Douglas A
 12 KHODAOUST, Mehran M
 14 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
 15 DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
 17 <130> FILE REFERENCE: 210147.0065/65US
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/766,511
 20 <141> CURRENT FILING DATE: 2001-01-19
 22 <150> PRIOR APPLICATION NUMBER: US 09/578,063
 23 <151> PRIOR FILING DATE: 2000-05-24
 25 <150> PRIOR APPLICATION NUMBER: US 09/333,159
 26 <151> PRIOR FILING DATE: 1999-06-14
 28 <150> PRIOR APPLICATION NUMBER: US 09/596,194
 29 <151> PRIOR FILING DATE: 2000-06-16
 31 <150> PRIOR APPLICATION NUMBER: US 09/342,364
 32 <151> PRIOR FILING DATE: 1999-06-29
 34 <150> PRIOR APPLICATION NUMBER: US 09/608,452
 35 <151> PRIOR FILING DATE: 2000-06-30
 37 <150> PRIOR APPLICATION NUMBER: US 09/393,996
 38 <151> PRIOR FILING DATE: 1999-09-10
 40 <150> PRIOR APPLICATION NUMBER: US 09/345,680
 41 <151> PRIOR FILING DATE: 1999-06-30
 43 <160> NUMBER OF SEQ ID NOS: 85
 45 <170> SOFTWARE: PatentIn Ver. 2.1
 47 <210> SEQ ID NO: 1
 48 <211> LENGTH: 2964
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Homo sapiens
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 55 ggacgcggagg agccatqagg cggccggctg cgaagggtggc ggcgtctqctq ctggggctgc 180
 56 tcttggatgt cacagaagcc aaaaagcatl gctggatll cgaaggactc tatecaaccl 240
 57 attatataatc cggctccatc gaggactqct gtggctccag gtgtctgtgtg cggccctct 300
 58 ccatacagag gctgtgtac ttcgtgttcc ttctgtatgtat gggcgtgtgtt ttcgtgtgtc 360
 59 gagccggctt cttccatccgg aggccatgtt accccccccgc gctgtatcgag gagccaaqct 420
 60 tcaatgtgtc ctacaccagg cagcccccaa atcccgccgc aggagcccaag cagccggggc 480
 61 cggccatataa cactgaccca ggaggacccg ggtgtgtgtt tccatggca 540
 62 tggcttca ggtccccccc aactcacccc aggggagtgt ggcctgcccgg cccctcccaag 600
 63 cctactgcaaa caccgttccg ccccgatcag aacaggtagt gaaaggccaaag tagtgggggtg 660

Does Not Comply
 Corrected Diskette Needed
 See Attachment
 Last page

RAW SEQUENCE LISTING DATE: 02/05/2001
PATENT APPLICATION: US/09/766,511 TIME: 13:34:39

Input Set : A:\10147_61.txt
Output Set: N:\CRF3\02052001\I766511.raw

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 65 gttcaetcc aggaacggc tctgtggctg ctaagggcag ttccctctgat atccctcag 780
 66 caaqcacagc tctcttcaq qcttccatq gactacaata tataactacta cacttttgtt 840
 67 ectctgttc ttctgtttc gacgcaatctg tgctctcact atggtagtgt ggtgacatc 900
 68 cccqagggtt gacgtctta cggtggcgtt acaggatctt caggagagag actqagqaga 960
 69 agaaggcagt gctggaggly caggtygcat gtagaggggc caggccgagc atccccggca 1020
 70 aqcatcttc tqcccgqta ttaataqgaa gccccatqcc qqqcugctca gccqatqaaq 1080
 71 cagcagccga ctgacgtqaa cccqacggat catctgtcc aqctgtctt ctcgtcaac 1140
 72 ttcccttc aqaaactgtt gggagacat tcaaggagaga gcaagccctt tgtagtatt 1200
 73 ctgtcttgtt tcatatctta aqaaatqact tccctcgac cyccaggaa qggtagcag 1260
 74 ttcacgttcc acccaggat ggggctatg atcaggctt ccttggggc ctgacatgtt 1320
 75 tctqacatcc actaaqcaaa ttatattaa ttcatggaa atcacttctt gccccaaact 1380
 76 qagacattgc attttqgtqaa ctcttggctt gatttggaga aaggactqtt accccatttt 1440
 77 ttggtqgtqtt tataqgatq catqtagacg gtcctgcctt tttaaatctg acttgggtgt 1500
 78 tttttttttt qyaatcaact gctcttcggc gycatttca ggccttgggg ttccttcc 1560
 79 ttcqccagctt ccqatgggtq gttctgttcaaa gtccttccaa aacggggcact attcqgtctq 1620
 80 qaaqtcacat qqactcttcc agggagagaq accaaqctqaa gctctctctt ctgagggtgt 1680
 81 qttggqlcta aqggggltgt tttttgggtt caaqgaggag gagcttgcgtt qaaaaagaca 1740
 82 qqagaqgtac tttttttttt gcaatqaccat tttttttttt tttttttttt tttttttttt 1800
 83 qtcggqaatq caccatctt gataqgaaatc acqatcttcc ccaqatcttcc acaggqatgc 1860
 84 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1920
 85 qtgaaqctgtt accttgcctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1980
 86 actatqatgtt ctgtatcacc gggaaatgggg tttttttttt tttttttttt tttttttttt 2040
 87 agagccctttt gaaaatqatq tttttttttt tttttttttt tttttttttt tttttttttt 2100
 88 qatacqggat gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2160
 89 ctggggaaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2220
 90 aqccacatqat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2280
 91 qttttttttt atqatqatq tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2340
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 93 cattttttat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2460
 94 qtgcagctga ataggcaccat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2520
 95 uattatgtta aqagacatq tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2580
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 100 qttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2880
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 102 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2964
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 104 <211> LENGTH: 516
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 106 <213> ORGANISM: Homo sapiens
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 109 qaagaaaaaa aqacttgcgtt gtatttcgaa ggacttctat caacccatata tataatccgc 120
 110 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 180
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RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/766,511 TIME: 13:34:39

Input Set : A:\10147_61.txt
 Output Set: N:\CRF3\02052001\I766511.raw

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 117 gacccagag gaccgggat gaaccctgtc gggaaattcca tggcaatggc tticcagggtc 420
 118 ccacccaact caccgggg qagtgtggcc tggccccccttccagcccttctgaaacacg 480
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 123 <211> LENGTH: 172
 124 <212> TYPE: PRT
 125 <213> ORGANISM: Homo sapiens
 127 <400> SEQUENCE: 3
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 130 Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
 131 20 25 30
 132 Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
 133 35 40 45
 134 Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
 135 50 55 60
 136 Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
 137 65 70 75 80
 138 Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
 139 85 90 95
 140 Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
 141 100 105 110
 142 Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
 143 115 120 125
 144 Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
 145 130 135 140
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 157 Leu Glu Cys Thr Glu Ala
 158 20
 159 <210> SEQ ID NO: 5
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 161 <212> TYPE: PRT
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 163 <400> SEQUENCE: 5
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 165 1 5 10 15
 166 Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg Cys Cys Val Arg Ala
 167 20 25 30

RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/766,511 TIME: 13:34:39

Input Set : A:\10147_61.txt
 Output Set: N:\CRF3\02052001\I766511.raw

187 Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe Leu Leu Met Met Gly
 188 35 40 45
 190 Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile Arg Arg Arg Met Tyr
 191 50 55 60
 193 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
 194 65 70 75 80
 196 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
 197 85 90 95
 199 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
 200 100 105 110
 202 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
 203 115 120 125
 205 Cys Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
 206 130 135 140
 208 Gln Val Val Lys Ala Lys
 209 145 150
 212 <210> SEQ ID NO: 6
 213 <211> LENGTH: 38
 214 <212> TYPE: PRT
 215 <213> ORGANISM: Homo sapiens
 217 <400> SEQUENCE: 6
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 221 Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg Cys Cys Val Arg Ala
 222 20 25 30
 224 Leu Ser Ile Gln Arg Leu
 225 35
 228 <210> SEQ ID NO: 7
 229 <211> LENGTH: 21
 230 <212> TYPE: PRT
 231 <213> ORGANISM: Homo sapiens
 233 <400> SEQUENCE: 7
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 235 1 5 10 15
 237 Ala Gly Phe Phe Ile
 238 20
 241 <210> SEQ ID NO: 8
 242 <211> LENGTH: 91
 243 <212> TYPE: PRT
 244 <213> ORGANISM: Homo sapiens
 246 <400> SEQUENCE: 8
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 248 1 5 10 15
 250 Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
 251 20 25 30
 253 Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Pro Gly Met Asn Pro
 254 35 40 45
 256 Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
 257 50 55 60

RAW SEQUENCE LISTING DATE: 02/05/2001
PATENT APPLICATION: US/09/766,511 TIME: 13:34:39

Input Set : A:\10147_61.txt
Output Set: N:\CRF3\02052001\1766511.raw

Attachment

Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala
100 105 110

His Leu Val Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln
115 120 125

Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln
130 135 140

Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn
145 150 155 160

Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys
165 170 175

Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val
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Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr
195 200 205

Leu

<210> 61
<211> 821
<212> DNA
<213> Mus sp.

see item #10 on ERROR SUMMARY
Report. Use of "n" requires numeric
identifiers <2207>, <2217>, <2227>, and <2237>.

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attttggaga cagatgcaag aaacccctga ccttctgaac atacaccta acaatggtgc 180
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tgatttccat gttactctt agtacactgtt tcattgcgag ctgtgtgggt acttaccaat 300
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gtgagcagaa ctgtgttcag atgggggctc atctgggtt gatcaataact gaagcggagc 540
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ccaaaggtaat ggcaaatggc aatggatcga tgataactcct ttcagtcaaa atgtcagggtt 660
ctggcaccccc catgaaccca atcttccaga agagcgggtt gtttcaatag tttactggaa 720
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<210> 62

<211> 534

<212> DNA

<213> Mus sp.

<400> 62

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taccaattta ttatggacca gcccagtata agactatatg aacctcacac ataccattcc 180
agtctcacct gtttcagatc aaggactatg gtgtcagaaa aaatgtgggg atgctggccca 240
aatcacttgg agtcatgtt ctccagctgc tacctcattt ctaccaagga gaacttctgg 300
agcaccatgtc agcagaactg tggtcagatg ggggctcatc tgggtgtat caatactgaa 360
gcggagcaga atttcatcac ccagcagctg aatgagtcac tttcttactt cctgggtctt 420

VERIFICATION SUMMARY DATE: 02/05/2001
 PATENT APPLICATION: US/09/766,511 TIME: 13:34:40

Input Set : A:\10147_61.txt
 Output Set: N:\CRF3\02052001\I766511.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:267 M:283 W: Missing Blank Line separator, <400> field identifier
 L:268 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
 L:272 M:283 W: Missing Blank Line separator, <400> field identifier
 L:273 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
 L:391 M:283 W: Missing Blank Line separator, <400> field identifier
 L:392 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
 L:433 M:283 W: Missing Blank Line separator, <400> field identifier
 L:434 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
 L:438 M:283 W: Missing Blank Line separator, <400> field identifier
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 L:443 M:283 W: Missing Blank Line separator, <400> field identifier
 L:444 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
 L:448 M:283 W: Missing Blank Line separator, <400> field identifier
 L:449 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
 L:453 M:283 W: Missing Blank Line separator, <400> field identifier
 L:454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
 L:1749 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1750 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
 L:1754 M:283 W: Missing Blank Line separator, <400> field identifier
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 L:1896 M:283 W: Missing Blank Line separator, <400> field identifier
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 L:1901 M:283 W: Missing Blank Line separator, <400> field identifier
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 L:1907 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
 L:1911 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1912 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
 L:1916 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
 L:1921 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1922 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
 L:1926 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1927 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
 L:2118 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2119 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
 L:2123 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:
 L:2128 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2129 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE:
 L:2133 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (59) SEQUENCE:
 L:2205 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
 L:2205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
 L:2205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
 L:2205 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61
 L:2205 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61

VERIFICATION SUMMARY DATE: 02/05/2001

PATENT APPLICATION: US/09/766,511 TIME: 13:34:40

Input Set : A:\10147_61.txt

Output Set: N:\CRF3\02052001\1766511.raw

L:2322 M:283 W: Missing Blank Line separator, <400> field identifier
L:2323 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:2327 M:283 W: Missing Blank Line separator, <400> field identifier
L:2328 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:2332 M:283 W: Missing Blank Line separator, <400> field identifier
L:2333 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:2337 M:283 W: Missing Blank Line separator, <400> field identifier
L:2338 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:2342 M:283 W: Missing Blank Line separator, <400> field identifier
L:2343 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:2513 M:283 W: Missing Blank Line separator, <400> field identifier
L:2514 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:
L:2518 M:283 W: Missing Blank Line separator, <400> field identifier
L:2519 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (75) SEQUENCE:
L:2523 M:283 W: Missing Blank Line separator, <400> field identifier
L:2524 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:
L:2528 M:283 W: Missing Blank Line separator, <400> field identifier
L:2529 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:
L:2533 M:283 W: Missing Blank Line separator, <400> field identifier
L:2534 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:
L:2538 M:283 W: Missing Blank Line separator, <400> field identifier
L:2539 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:2543 M:283 W: Missing Blank Line separator, <400> field identifier
L:2544 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE: